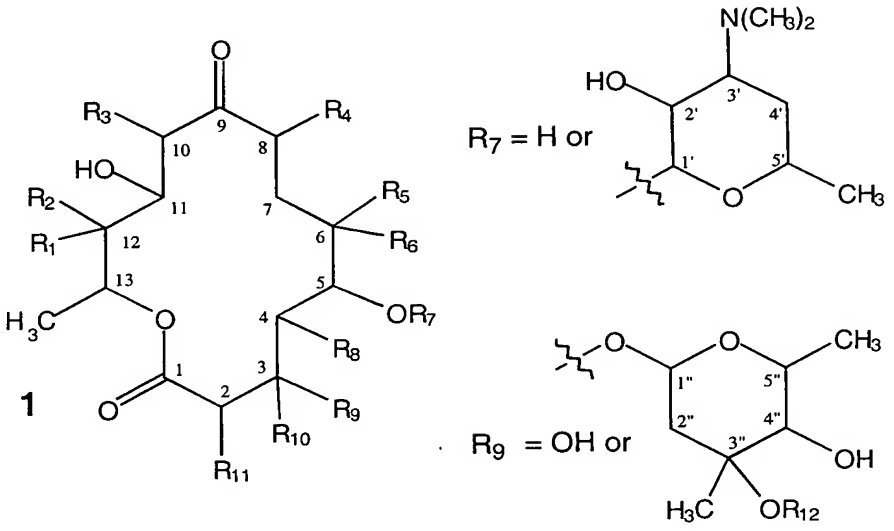
Amendments to the Claims:

Claims 1-26 (Cancelled)

Claim 27 (Currently Amended): A process for the production of compounds of formula **1**:



and to pharmaceutically acceptable salts thereof, wherein:

R_1 is H or OH; R_2-R_4 are each independently H, CH_3, or CH_2CH_3; R_5 is H or OH; and R_6 is H, CH_3, or CH_2CH_3; R_7 is H or desosamine; R_8 is H, CH_3, or CH_2CH_3; R_9 is OH, mycarose (R_{12} is H), or cladinose (R_{12} is CH_3), R_{10} is H; or R_9 = R_{10} = O; and R_{11} is H, CH_3, or CH_2CH_3, with the proviso that when R_2-R_4 are CH_3, R_6 is CH_3, R_8 is CH_3, and R_{11} is CH_3, then R_1 and R_5 are not H and R_{12} is not H; or also when R_2-R_4 are CH_3, R_6 is CH_3, R_8 is CH_3, and R_{11} is CH_3, then R_1 and R_5 are not OH and R_{12} is not H;

said process comprising culturing a transformant organism which contains a DNA gene assembly which produces a 14-membered macrolide, said gene assembly comprising a loading module of the form KSq-ATq-ACP where:

a) KSq represents a domain operative to decarboxylate a malonate substrate carried by the ACP;

b) ATq represents an acyltransferase domain operative to load selectively a malonate unit onto the ACP; and

c) ACP represents an acyl carrier protein

and a plurality of extension modules, wherein said extension modules are not usually associated with a loading module that effects decarboxylation of a malonyl residue.

Claim 28 (Previously Presented): The process of claim 27, wherein the loading module is selected from the oleandomycin, spiramycin, niddamycin, methymycin or monensin PKSs.

Claim 29 (Currently Amended): The process of claim 27, wherein the plurality of extension modules correspond to the extension modules of a PKS selected from the group consisting of erythromycin, ~~PKS~~ narbomycin, pikromycin, lankamycin, kujimycin, and megalomycin.

Claim 30 (Previously Presented): The process of claim 28, wherein the plurality of extension modules correspond to the extension modules of the erythromycin PKS.

Claim 31 (Previously Presented): The process of claim 27, wherein the organism is selected from the group consisting of: *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces longisporoflavus*, *Streptomyces hygroscopicus*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, and *Streptomyces tsukubaensis*.

Claim 32 (Previously Presented): The process of claim 28, wherein the organism is selected from the group consisting of: *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces*

longisporoflavus, *Streptomyces hygroscopicus*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, and *Streptomyces tsukubaensis*.

Claim 33 (Previously Presented): The process of claim 29, wherein the organism is selected from the group consisting of: *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces longisporoflavus*, *Streptomyces hygroscopicus*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, and *Streptomyces tsukubaensis*.

Claim 34 (Previously Presented): The process of claim 30, wherein the organism is selected from the group consisting of: *Saccharopolyspora erythraea*, *Streptomyces coelicolor*, *Streptomyces avermitilis*, *Streptomyces griseofuscus*, *Streptomyces cinnamonensis*, *Streptomyces fradiae*, *Streptomyces longisporoflavus*, *Streptomyces hygroscopicus*, *Micromonospora griseorubida*, *Streptomyces lasaliensis*, *Streptomyces venezuelae*, *Streptomyces antibioticus*, *Streptomyces lividans*, *Streptomyces rimosus*, *Streptomyces albus*, *Amycolatopsis mediterranei*, and *Streptomyces tsukubaensis*.

Claim 35 (Currently Amended): The process of claim 27, which additionally comprises recovering the compound produced by said process ~~a compound of formula 1~~.

Claim 36 (New): The process of claim 27, wherein said compound is 15-norerythromycin A.

Claim 37 (New): The process of claim 27, wherein said compound is 15-norerythromycin B.

Claim 38 (New): The process of claim 27, wherein said KSq domain is obtained by replacing the active site cysteine of a KS domain of an extension module with a glutamine.

Claim 39 (New): The process of claim 27, wherein said ATq domain is obtained by replacing the active site residue of an AT domain of an extension module with an arginine.